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SEQUENCE LISTING

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 The University of Queensland

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Glu	Trp	Ser 35	Arg	Gl'n	Trp	Gl'n	Gly 40	Thr	Glu	Gly	Asn	Gly 45	His	Ala	Āla	
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Ala	Ser	Gly	Ile	Pro	Gly	Leu	Asp	Ala	Leu	Ala	Gly	Val	Lys	Ile	Ala	192
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Pro Ala Gln Leu Gly Asp Ile Gln Gln Arg Tyr Met Lys Asp Phe Ser

Ala Leu Trp Gln Ala Met Ala Glu Gly Lys Ala Glu Ala Thr Gly Pro · 90

Leu His Asp Arg Arg Phe Ala Gly Asp Ala Trp Arg Thr Asn Leu Pro

Tyr Arg Phe Ala Ala Ala Phe Tyr Leu Leu Asn Ala Arg Ala Leu Thr

Glu Leu Ala Asp Ala Val Glu\ Ala Asp Ala Lys Thr Arg Gln Arg Ile 135

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Leu Ala Ser Ile Asp Val Pro Thr Tyr Ile Tyr Gly Ser Arg Glu Asp 465 470 475 480

His Ile Val Pro Trp Thr Ala Ala Tyr Ala Ser Thr Ala Leu Leu Ala 485 490 495

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- 17 - .

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Ser Arg Gly Gln Ser Ala Ala Met Ala Pro Phe Gly Gly Leu Lys Ser 20 25 30	
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Met Thr Gly Phe Pro Val Lys Lys Val Asn Thr Asp Ile Thr Ser Ile 35 40 45	
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55 55 60	
gga aag aag attt gag act ctt tcc tat ttg cca cca ttg acc aga Gly Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg	240
65 70 75 Led Fro Fro Led Thr Arg	
gat too egg gtg act gac gtt gtc atc gta too gcc gcc egc acc gcg	288
Asp Ser Arg Val Thr Asp Val Val Ile Val Ser Ala Ala Arg Thr Ala 85 90 95	
gtc ggc aag ttt ggc ggc tcg ctg gcc aag atc ccg gca ccg gaa ctg Val Gly Lys Phe Gly Gly Ser Leu Ala Lys Ile Pro Ala Pro Glu Leu	336
100 105 110 Pro Ara Pro Giu Leu	
ggt gcc gtg gtc atc aag gcc gcg ctg gag cgc gcc ggc gtc aag ccg Gly Ala Val Val Ile Lys Ala Ala Leu Glu Arg Ala Gly Val Lys Pro	384
115 120 125	
gag cag gtg agc gaa gtc atc atg ggc cag gtg ctg acc gcc ggt tcg Glu Gln Val Ser Glu Val Ile Met Gly Gln Val Leu Thr Ala Gly Ser	432
and any top one ore the mer ork orm hat ned the war did set	•

- 18 -

	130					135					140					
ggc Gly 145	cag Gln	aac Asn	ccc Pro	gca Ala	cgc Arg 150	cag Gln	gcc Ala	gcg Ala	atc Ile	aag Lys 155	gcc Ala	GJ y ggc	ctg Leu	ccg Pro	gcg Ala 160	. 480
				atg Met 165												528
				gcc Ala												576
				ggc Gly							Ala					624
				gat Asp												672
				gac Asp												720
				gag Glu 245												768
				ttc Phe								Ala				816
	Lys			aag Lys												864
				gac Asp												912
				ctg Leu												960
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50

ccc Pro	aag Lys 370	gtg Val	atg Met	ggc Gly	atg Met	ggc Gly 375	ccg Pro	gtg Val	ccg Pro	gcc Ala	tcc Ser 380	aag Lys	cgc Arg	gcc Ala	ctg Leu	1152
tcg Ser 385	cgc Arg	gcc Ala	gag Glu	tgg Trp	acc Thr 390	ccg Pro	caa Gln	gac Asp	ctg Leu	gac Asp 395	ctg Leu	atg Met	gag Glu	atc Ile	aac Asn 400	1200
gag Glu	gcc Ala	ttt Phe	gcc Ala	gcc Ala 405	cag Gln	gcg Ala	ctg Leu	gcg Ala	gtg Val 410	cac His	cag Gln	cag Gln	atg Met	ggc Gly 415	tgg Trp	1248
gac Asp	acc Thr	tcc Ser	aag Lys 420	gtc Val	aat Asn	gtg Val	aac Asn	ggc Gly 425	Gly ggc	gcc Ala	atc Ile	gcc Ala	atc Ile 430	ggc Gly	cac His	1296
ccg Pro	atc Ile	ggc Gly 435	gcg Ala	tcg Ser	ggc Gly	tgc Cys	cgt Arg 440	atc Ile	ctg Leu	gtg Val	acg Thr	ctg Leu 445	ctg Leu	cac His	gag Glu	1344
atg Met	aag Lys 450	cgc Arg	cgt Arg	gac Asp	gcg Ala	aag Lys 455	aag Lys	ggc Gly	ctg Leu	gcc Ala	tcg Ser 460	ctg Leu	tgc Cys	atc Ile	ggc Gly	1392
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Ser	Arg	Gly	Gln 20	Ser	Ala	Ala	Met	Ala 25	Pro	Phe	: Gly	Gly	Leu 30	Lys	Ser	
Met	Thr	: Gly 35	, Phe	Pro	Val	. Lys	Lys 40	val	. Asn	Thr	: Asp	11e 45	. Thr	Ser	lle	

Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile 50 60 .

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- Asp Ser Arg Val Thr Asp Val Val Ile Val Ser Ala Ala Arg Thr Ala 85 . 90 95
- Val Gly Lys Phe Gly Gly Ser Leu Ala Lys Ile Pro Ala Pro Glu Leu 100 105 110
- Gly Ala Val Val Ile Lys Ala Ala Leu Glu Arg Ala Gly Val Lys Pro 115 120 125
- Glu Gln Val Ser Glu Val Ile Met Gly Gln Val Leu Thr Ala Gly Ser 130 135 140
- Gly Gln Asn Pro Ala Arg Gln Ala Ala Ile Lys Ala Gly Leu Pro Ala 145 150 . 155 160
- Met Val Pro Ala Met Thr Ile Asn Lys Val Cys Gly Ser Gly Leu Lys 165 170 175
- Ala Val Met Leu Ala Ala Asn Ala Ile Met Ala Gly Asp Ala Glu Ile 180 185 190
- Val Val Ala Gly Gly Gln Glu Asn Met Ser Ala Ala Pro His Val Leu 195 200 . 205
- Pro Gly Asp Gly Phe Arg Met Gly Asp Ala Lys Leu Val Asp 210 215 220
- Thr Met Ile Val Asp Gly Leu Trp Asp Val Tyr Asn Gln Tyr His Met 225 230 235 240
- Gly Ile Thr Ala Glu Asn Val Ala Lys Glu Tyr Gly Ile Thr Arg Glu 245 250 255
- Ala Gln Asp Glu Phe Ala Val Gly Ser Gln Asn Lys Ala Glu Ala Ala 260 265 270
- Gln Lys Ala Gly Lys Phe Asp Glu Glu Ile Val Pro Val Leu Ile Pro 275 280 285

Gln Arg Lys Gly Asp Pro Val Ala Phe Lys Thr Asp Glu Phe Val Arg 290 295 300

Gln Gly Ala Thr Leu Asp Ser Met Ser Gly Leu Lys Pro Ala Phe Asp 305 310 315 320

Lys Ala Gly Thr Val Thr Ala Ala Asn Ala Ser Gly Leu Asn Asp Gly 325 330 335

Ala Ala Ala Val Val Met Ser Ala Ala Lys Ala Lys Glu Leu Gly 340 345 350

Leu Thr Pro Leu Ala Thr Ile Lys Ser Tyr Ala Asn Ala Gly Val Asp 355 . 360 365

Pro Lys Val Met Gly Met Gly Pro Val Pro Ala Ser Lys Arg Ala Leu 370 375 380

Ser Arg Ala Glu Trp Thr Pro Gln Asp Leu Asp Leu Met Glu Ile Asn 385 390 395 400

Glu Ala Phe Ala Ala Gln Ala Leu Ala Val His Gln Gln Met Gly Trp
405 410 415

Asp Thr Ser Lys Val Asn Val Asn Gly Gly Ala Ile Ala Ile Gly His
420 425 430

Pro Ile Gly Ala Ser Gly Cys Arg Ile Leu Val Thr Leu Leu His Glu

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- 24 -

145					150					155					160		
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gac Asp	gtg Val	gtg Val	ttc Phe 180	cgc Arg	aag Lys	atg Met	acc Thr	cgc Arg 185	gcc Ala	gac Asp	tgg Trp	gat Asp	gcg Ala 190	gtg Val	atc Ile		576
gac Asp	acc Thr	aac Asn 195	ctg Leu	acc Thr	tcg Ser	ctg Leu	ttc Phe 200	aac Asn	gtc Val	acc Thr	aag Lys	cag Gln 205	gtg Val	atc Ile	gac Asp		624
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Met Thr Gly Phe Pro Val Lys Lys Val Asn Thr Asp Ile Thr Ser Ile 35 40 45

Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile 50 55 60

Gly Lys Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg 65 70 75 80

Asp Ser Arg Val Thr Gln Arg Ile Ala Tyr Val Thr Gly Gly Met Gly 85 90 95

Gly Ile Gly Thr Ala Ile Cys Gln Arg Leu Ala Lys Asp Gly Phe Arg 100 105 110

Val Val Ala Gly Cys Gly Pro Asn Ser Pro Arg Arg Glu Lys Trp Leu 115 120 125

Glu Gln Gln Lys Ala Leu Gly Phe Asp Phe Ile Ala Ser Glu Gly Asn 130 135 140

Val Ala Asp Trp Asp Ser Thr Lys Thr Ala Phe Asp Lys Val Lys Ser 145 150 155 160

Glu Val Gly Glu Val Asp Val Leu Ile Asn Asn Ala Gly Ile Thr Arg 165 170 175

Asp Val Val Phe Arg Lys Met Thr Arg Ala Asp Trp Asp Ala Val Ile 180 185 190

Asp Thr Asn Leu Thr Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp 195 200 205

Gly Met Ala Asp Arg Gly Trp Gly Arg Ile Val Asn Ile Ser Ser Val 210 215 220

- 26 -

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Lys Gly Val Thr Val Asn Thr Val Ser Pro Gly Tyr Ile Ala Thr Asp 265 260

Met Val Lys Ala Ile Arg Gln Asp Val Leu Asp Lys Ile Val Ala Thr 275 280

Ile Pro Val Lys Arg Leu Gly Leu Pro Glu Glu Ile Ala Ser Ile Cys 295 290

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Ser Arg Gly Gln Ser Ala Ala Met Ala Pro Phe Gly Gly Leu Lys Ser 20 25 30	
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Met Thr Gly Phe Pro Val Lys Lys Val Asn Thr Asp Ile Thr Ser Ile 35 40 45	
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Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile 50 55 60	•
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Gly Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg	

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		tgg cag ggc act gaa g Trp Gln Gly Thr Glu G 125	
cac gcg gcc gcg tc His Ala Ala Ala Se 130	c ggc att ccg r Gly Ile Pro 135	ggc ctg gat gcg ctg o Gly Leu Asp Ala Leu A 140	gca ggc gtc 432 Ala Gly Val
aag atc gcg ccg gc Lys Ile Ala Pro Al 145	g cag ctg ggt a Gln Leu Gly 150	gat atc cag cag cgc t Asp Ile Gln Gln Arg 1 155	tac atg aag 480 Tyr Met Lys 160
gac ttc tca gcg ct Asp Phe Ser Ala Le 16	u Trp Gln Ala	atg gcc gag ggc aag g Met Ala Glu Gly Lys 1 170	gcc gag gcc 528 Ala Glu Ala 175
acc ggt ccg ctg ca Thr Gly Pro Leu Hi 180	c gac cgg cgc s Asp Arg Arg	ttc gcc ggc gac gca t Phe Ala Gly Asp Ala 1 185	agg age ace 576 Frp Arg Thr 190
		gcg ttc tac ctg ctc a Ala Phe Tyr Leu Leu 1 205	
		gtc gag gcc gat gcc a Val Glu Ala Asp Ala I 220	
		caa tgg gtc gat gcg a Gln Trp Val Asp Ala i 235	
	a Thr Asn Pro	gag gcg cag cgc ctg of Glu Ala Gln Arg Leu 1 250	
		ggc gtg cgc aac atg a Gly Val Arg Asn Met N 265	
		acc gac gag agc gcg f Thr Asp Glu Ser Ala 1 285	
		ggc gcc gtg gtc ttc (Gly Ala Val Val Phe (

tac Tyr 305	ttc Phe	cag Gln	ctg Leu	ttg Leu	cag Gln 310	tac Tyr	aag Lys	ccg Pro	ctg Leu	acc Thr 315	gac Asp	aag Lys	gtg Val	cac His	gcg Ala 320	960
cgc Arg	ccg Pro	ctg Leu	ctg Leu	atg Met 325	gtg Val	ccg Pro	ccg Pro	tgc Cys	atc Ile 330	aac Asn	aag Lys	tac Tyr	tac Tyr	atc Ile 335	ctg Leu	1008
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Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile 50 55 60

Gly Lys Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg
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Gly Lys Ser Gln Pro Phe Lys Val Thr Pro Gly Pro Phe Asp Pro Ala 100 105 110

Thr Trp Leu Glu Trp Ser Arg Gln Trp Gln Gly Thr Glu Gly Asn Gly 115 120 125

His Ala Ala Ala Ser Gly Ile Pro Gly Leu Asp Ala Leu Ala Gly Val 130 135 140

Lys Ile Ala Pro Ala Gln Leu Gly Asp Ile Gln Gln Arg Tyr Met Lys 145 150 155 160

Asp Phe Ser Ala Leu Trp Gln Ala Met Ala Glu Gly Lys Ala Glu Ala 165 170 175

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Gln Arg Ile Arg Phe Ala Ile Ser Gln Trp Val Asp Ala Met Ser Pro 225 230 235 240

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Ser Gly Gly Glu Ser Leu Arg Ala Gly Val Arg Asn Met Met Glu Asp

- 32 -

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Gly	Arg 290	Asn	Val	Ala	Val	Thr 295	Glu	Gly	Ala	Val	Val 300	Phe	Glu	Asn	Glu
Tyr 305	Phe	Gln	Leu	Leu	Gln 310	Tyr	Lys	Pro	Leu	Thr 315	Asp	Lys	Val	His	Ala 320
Arg	Pro	Leu	Leu	Met 325	Val	Pro	Pro	Cys	Ile 330	Asn	Lys	Tyr	Tyr	Ile 335	Leu
Asp	Leu	Gln	Pro 340	Glu	Ser	Ser	Leu	Val 345	Arg	His	Val	Val	Glu 350	Gln	Gly
His	Thr	Val 355	Phe	Leu	Val	Ser	Trp 360	Arg	Asn	Pro	Asp	Ala 365	Ser	Met	Ala
Gly	Ser 370	Thr	Trp	Asp	Asp	Tyr 375	Ile	Glu	His	Ala	Ala 380	Ile	Arg	Ala	Ile
Glu 385	Val	Ala	Arg	Asp	Ile 390	Ser	Gly	Gln	Asp	Lys 395	Ile	Asn	Val	Leu	Gly 400
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Ala	Arg	Gly	Glu 420	His	Pro	Ala	Ala	Ser 425	Val	Thr	Leu	Leu	Thr 430	Thr	Leu
Leu	-	Phe -435	Ala	Asp	Thr	Gly	Ile 440	Leu	Asp	Val	Phe	Val 445	Asp	Glu	Gly
His	Val 450	Gln	Leu	Arg	Glu	Ala 455	Thr	Leu	Gly	Gly	Gly 460	Ala	Gly	Ala	Pro
Cys 465	Ala	Leu	Leu	Arg	Gly 470	Leu	Glu	Leu	Ala	Asn 475	Thr	Phe	Ser	Phe	Leu 480
Arg	Pro	Asn	Asp	Leu 485	Val	Trp	Asn	Tyr	Val 490	Val	Asp	Asn	Tyr	Leu 495	Lÿs

•

Gly Asn Thr Pro Val Pro Phe Asp Leu Leu Phe Trp Asn Gly Asp Ala 500 505 510

Thr Asn Leu Pro Gly Pro Trp Tyr Cys Trp Tyr Leu Arg His Thr Tyr 515 520 525

Leu Gln Asn Glu Leu Lys Val Pro Gly Lys Leu Thr Val Cys Gly Val 530 535 540

Pro Val Asp Leu Ala Ser Ile Asp Val Pro Thr Tyr Ile Tyr Gly Ser 545 550 555 560

Arg Glu Asp His Ile Val Pro Trp Thr Ala Ala Tyr Ala Ser Thr Ala 565 570 575

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Ala Gly Val Ile Asn Pro Pro Ala Lys Asn Lys Arg Ser His Trp Thr 595 600 605

Asn Asp Ala Leu Pro Glu Ser Pro Gln Gln Trp Leu Ala Gly Ala Ile 610 615 620

Glu His His Gly Ser Trp Trp Pro Asp Trp Thr Ala Trp Leu Ala Gly 625 630 635 640

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ace tee geg ege atg gte etg	ctc cag gcg gtg	cgc cag ccg ct	g cac 144
Thr Ser Ala Arg Met Val Leu : 35	Leu Gin Ala Val 40	45	u nis
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Ser Ala Arg His Val Ala His 50 55	Phe Ser Leu Glu	. Leu Lys Asn Va 60	ıl Leu
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Leu Gly Gln Ser Glu Leu Arg	Pro Gly Asp Asp	Asp Arg Arg Ph	ne Ser 80
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85 _.	90	. 95	

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cg(Ar	tco g Sei 530	: Gly	aaç Y Lys	aco Thi	c cgc	aaq J Lys 535	s Ala	g cco	gco Ala	ago a Ser	cto Lev 540	ı Gly	aac Asn	aaq Lys	g acc s Thr	1632
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170

165

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120

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Pro	Ile	Asp 435	Leu	Lys	Gln	Val	Thr 440	Cys	_Asp	Phe	Tyr	Cys 445	Val	Ala	Gly
Leu	Asn 450	Asp	His	Ile	Thr	Pro 455	Trp	Glu	Ser	Суз	Tyr 460	Lys	Ser	Ala	Arg
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Gln	Ser	Ile	Leu	Asn 485	Pro	Pro	Gly	Asn	Pro 490	Lys	Ala	Arg	Phe	Met 495	Thr
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Lys	His	Ala 515		Ser	Trp	Trp	Leu 520		Trp	Gln	Gln	Trp 525	Leu	Ala	Glu
Arg	Ser 530		Lys	Thr	Arg	Lys 535		Pro	Ala	Ser	Leu 540	Gly	Asn	Lys	Thr
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acç Thr	g ago	g ccq	g gga 5 Gly 580	Ala	gct A Ala	gga Gly	a ato / Met	g gg Gly 58	y GII	a ggg ı Gly	g act	t ago r Sei	c ctt Lei 590	ı va.	g gtg l Val	1776
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- 45 -

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Tyr Leu Ala Trp Arg Lys Glu Leu His Ser Trp Ile Ser His Ser Asp . 100 105

Leu Ser Pro Gln Asp Ile Ser Arg Gly Gln Phe Val Ile Asn Leu Leu 120 115

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- 46 -

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- Ser Gln Val Asp Met Asp Ala Phe Glu Val Gly Lys Asn Leu Ala Thr 260 265 270
- Thr Glu Gly Ala Val Val Phe Arg Asn Asp Val Leu Glu Leu Ile Gln 275 280 285
- Tyr Arg Pro Ile Thr Glu Ser Val His Glu Arg Pro Leu Leu Val Val 290 295 300

Pro Pro Gln Ile Asn Lys Phe Tyr Val Phe Asp Leu Ser Pro Asp Lys 315 310 Ser Leu Ala Arg Phe Cys Leu Arg Asn Gly Val Gln Thr Phe Ile Val 330 Ser Trp Arg Asn Pro Thr Lys Ser Gln Arg Glu Trp Gly Leu Thr Thr 340 345 Tyr Ile Glu Ala Leu Lys Glu Ala Ile Glu Val Val Leu Ser Ile Thr Gly Ser Lys Asp Leu Asn Leu Leu Gly Ala Cys Ser Gly Gly Ile Thr Thr Ala Thr Leu Val Gly His Tyr Val Ala Ser Gly Glu Lys Lys Val 390 Asn Ala Phe Thr Gln Leu Val Ser Val Leu Asp Phe Glu Leu Asn Thr Gln Val Ala Leu Phe Ala Asp Glu Lys Thr Leu Glu Ala Ala Lys Arg 420 Arg Ser Tyr Gln Ser Gly Val Leu Glu Gly Lys Asp Met Ala Lys Val 435 Phe Ala Trp Met Arg Pro Asn Asp Leu Ile Trp Asn Tyr Trp Val Asn 455 Asn Tyr Leu Leu Gly Asn Gln Pro Pro Ala Phe Asp Ile Leu Tyr Trp 470 475 Asn Asn Asp Thr Thr Arg Leu Pro Ala Ala Leu His Gly Glu Phe Val Glu Leu Phe Lys Ser Asn Pro Leu Asn Arg Pro Gly Ala Leu Glu Val 500 Ser Gly Thr Pro Ile Asp Leu Lys Gln Val Thr Cys Asp Phe Tyr Cys 520 -515

Val Ala Gly Leu Asn Asp His Ile Thr Pro Trp Glu Ser Cys Tyr Lys

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Ser 545	Ala	Arg	Leu	Leu	Gly 550	Gly	Lys	Cys	Glu	Phe 555	Ile	Leu	Ser	Asn	Ser 560		
Gly	His	Ile	Gln	Ser 565	Ile	Leu	Asn	Pro	Pro 570	Gly	Asn	Pro	Lys	Ala 575	Arg		
Phe	Met	Thr	Asn 580	Pro	Glu	Leu	Pro	Ala 585	Glu	Pro	Lys	Ala	Trp 590	Leu	Glu		
Gln	Ala	Gly 595	Lys	His	Ala	Asp	Ser 600	Trp	Trp	Leu	His	Trp 605	Gln	Gln	Trp		
Leu	Ala 610	Glu	Arg	Ser	Gly	Lys 615	Thr	Arg	Lys	Ala	Pro 620	Ala	Ser	Leu	Gly		
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420

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<212> DNA

<213> Pseudomonas putida

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								gtc Val								1	.44
aca Thr	agc Ser 50	aat Asn	ggt Gly	gga Gly	aga Arg	gta Val 55	aag Lys	tgc Cys	atg Met	cag Gln	gtg Val 60	tgg Trp	cct Pro	cca Pro	aťt Ile	1	.92
gga Gly 65	aag Lys	aag Lys	aag Lys	ttt Phe	gag Glu 70	act Thr	ctt Leu	tcc Ser	tat Tyr	ttg Leu 75	cca Pro	cca Pro	ttg Leu	acc Thr	aga Arg 80	2	240
gat Asp	tcc Ser	Arg Arg	gtg Val	agg Arg 85	cca Pro	gaa Glu	atc Ile	gct Ala	gta Val 90	ctt Leu	gat Asp	atc Ile	caa Gln	ggt Gly 95	cag Gln	2	288
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atc Ile	atc Ile	ctg Leu 115	atc Ile	aac Asn	ggc Gly	tcg Ser	ctg Leu 120	gcc Ala	acc Thr	acg Thr	gcc Ala	tcg Ser 125	ttc Phe	gcc Ala	cag Gln	3	384
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ccg Pro 145	tat Tyr	tca Ser	ggc	aag Lys	tcc Ser 150	aag Lys	ccg Pro	cac His	aac Asn	cgt Arg 155	cag Gln	gaa Glu	cgg Arg	ctg Leu	atc Ile 160		180
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ctg Leu	gcg Ala	ctg Leu 195	gcg Ala	cac His	cag Gln	ccg Pro	cgg Arg 200	tac Tyr	gtg Val	aag Lys	гĀг	gca Ala 205	gtg Val	gtg Val	agt Ser	624
tcg Ser	ttc Phe 210	tcg Ser	cca Pro	gtg Val	atc Ile	aac Asn 215	gag Glu	ccg Pro	atg Met	cgc Arg	gac Asp 220	tat Tyr	ctg Leu	gac Asp	cgt Arg	672
ggc Gly 225	tgc Cys	cag Gln	tac Tyr	ctg Leu	gcc Ala 230	gcc Ala	tgc Cys	gac Asp	cgt Arg	tat Tyr 235	cag Gln	gtc Val	Gly ggc	aac Asn	ctg Leu 240	720
gtc Val	aat Asn	gac Asp	acc Thr	atc Ile 245	ggc Gly	aag Lys	cac His	ttg Leu	ccg Pro 250	tcg Ser	ctg Leu	ttc Phe	aaa Lys	cgc Arg 255	ttc Phe	768
aac Asn	tac Tyr	cgc Arg	cat His 260	gtg Val	agc Ser	agc Ser	ctg Leu	gac Asp 265	agc Ser	cac His	gag Glu	tac Tyr	gca Ala 270	cag Gln	atg Met .	816
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caa Gln	ggc Gly 290	gcg Ala	cgc Arg	aat Asn	atc Ile	aac Asn 295	atc Ile	ccg Pro	gtg Val	ctg Leu	ttc Phe 300	тте	aac Asn	Gly	gag Glu	912
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Val	Gly	Arg	Ser	Gln 325	Phe	Ser	Val	Ile	330	Asp	Ala	. СТУ	HIS	335		1008
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<213> Pseudomonas putida

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Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile 55

Gly Lys Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg

Asp Ser Arg Val Arg Pro Glu Ile Ala Val Leu Asp Ile Gln Gly Gln 90

Tyr Arg Val Tyr Thr Glu Phe Tyr Arg Ala Asp Ala Ala Glu Asn Thr

Ile Ile Leu Ile Asn Gly Ser Leu Ala Thr Thr Ala Ser Phe Ala Gln 120

Thr Val Arg Asn Leu His Pro Gln Phe Asn Val Val Leu Phe Asp Gln 135 130

Pro Tyr Ser Gly Lys Ser Lys Pro His Asn Arg Gln Glu Arg Leu Ile 150 155 145

Ser Lys Glu Thr Glu Ala His Ile Leu Leu Glu Leu Ile Glu His Phe 170 165

Gln Ala Asp His Val Met Ser Phe Ser Trp Gly Gly Ala Ser Thr Leu 185 180

Leu Ala Leu Ala His Gln Pro Arg Tyr Val Lys Lys Ala Val Val Ser 195 200 205

Ser Phe Ser Pro Val Ile Asn Glu Pro Met Arg Asp Tyr Leu Asp Arg 210 · 215 220

Gly Cys Gln Tyr Leu Ala Ala Cys Asp Arg Tyr Gln Val Gly Asn Leu 225 230 235 240

Val Asn Asp Thr Ile Gly Lys His Leu Pro Ser Leu Phe Lys Arg Phe 245 250 255

Asn Tyr Arg His Val Ser Ser Leu Asp Ser His Glu Tyr Ala Gln Met 260 265 270

His Phe His Ile Asn Gln Val Leu Glu His Asp Leu Glu Arg Ala Leu 275 280 285

Gln Gly Ala Arg Asn Ile Asn Ile Pro Val Leu Phe Ile Asn Gly Glu 290 295 300

Arg Asp Glu Tyr Thr Thr Val Glu Asp Ala Arg Gln Phe Ser Lys His 305 310 315 320

Val Gly Arg Ser Gln Phe Ser Val Ile Arg Asp Ala Gly His Phe Leu 325 330 335

Asp Met Clu Asn Lys Thr Ala Cys Glu Asn Thr Arg Asn Val Met Leu 340 345 350

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caggtgtggc	ctccaattgg	aaagaagaag	tttgagactc	tttcctattt	gccaccattg	240
accagagatt	cccgggtgag	gccagaaatc	gctgtacttg	atatccaagg	tcagtatcgg	300
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<210> 31

<211> 519

<212> DNA

<213> Aeromonas caviae

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<221> CDS

<222> (1)..(519)

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gag Glu	cgg Arg 50	ccc Pro	ata Ile	gtc Val	cac His	ggc Gly 55	atg Met	ctg Leu	ctc Leu	gcc Ala	agc Ser 60	ctc Leu	ttc Phe	tcc Ser	GJA āāā	192
ctg Leu 65	ctg Leu	ggc Gly	cag Gln	cag Gln	ttg Leu 70	ccg Pro	ggc Gly	aag Lys	GJÀ āāā	agc Ser 75	atc Ile	tat Tyr	ctg Leu	ggt Gly	caa Gln 80	240
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gag Glu	gtg Val	gag Glu	gtg Val 100	Thr	gcc Ala	ctt Leu	cgc Arg	gag Glu 105	gac · Asp	aag Lys	ccc Pro	atc Ile	gcc Ala 110	acc Thr	ctg Leu	336
acc Thr	acc	cgc Arg 115	Ile	ttc Phe	acc Thr	caa Gln	ggc Gly 120	Gly	gcc Ala	ctc Leu	gcc Ala	gtg Val 125	acg Thr	GJ À ààà	gaa Glu	384
gcc Ala	gtg Val 130	Val	aag Lys	ctg Leu	cct Pro	tca Ser 135	Lys	gct Ala	ttg Leu	ggc	aaa Lys 140	ggt Gly	gtt Val	acc Thr	gag Glu	432
gaa Glu 145	Gln	ttc Phe	aaa Lys	gag Glu	acc Thr 150	Trp	acg Thr	agg Arg	ccg Pro	gga Gly 155	Ala	gct Ala	gga Gly	atg Met	ggc Gly 160	480
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<212> PRT

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Phe Asn Pro Leu His Leu Asp Pro Ala Phe Ala Ala Thr Thr Ala Phe 40

Glu Arg Pro Ile Val His Gly Met Leu Leu Ala Ser Leu Phe Ser Gly

Leu Leu Gly Gln Gln Leu Pro Gly Lys Gly Ser Ile Tyr Leu Gly Gin

Ser Leu Ser Phe Lys Leu Pro Val Phe Val Gly Asp Glu Val Thr Ala

Glu Val Glu Val Thr Ala Leu Arg Glu Asp Lys Pro Ile Ala Thr Leu

Thr Thr Arg Ile Phe Thr Gln Gly Gly Ala Leu Ala Val Thr Gly Glu

Ala Val Val Lys Leu Pro Ser Lys Ala Leu Gly Lys Gly Val Thr Glu 135 130

Glu Gln Phe Lys Glu Thr Trp Thr Arg Pro Gly Ala Ala Gly Met Gly 155 150 145

Glu Gly Thr Ser Leu Val Val Ala Lys Ser Arg Met 165

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<211> 598

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<213> Aeromonas caviae

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<211> 31

<212> DNA

<213> artificial sequence

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<221> misc_feature

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